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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/928,847B

DATE: 05/16/2002 P-6
TIME: 14:10:20

Input Set : A:\10022204.ST25.txt

Output Set: N:\CRF3\05162002\I928847B.raw

3 <110> APPLICANT: Novozymes A/S
 4 Jorgensen, Steen T
 5 Rasmussen, Michael D
 6 Andersen, Jens Tonne
 7 Olsen, Carsten
 9 <120> TITLE OF INVENTION: Multiple Insertion of Genes
 11 <130> FILE REFERENCE: 10022.204-US
 13 <140> CURRENT APPLICATION NUMBER: 09/928847B
 C--> 14 <141> CURRENT FILING DATE: 2002-05-06
 16 <160> NUMBER OF SEQ ID NOS: 50
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 30
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Primer
 28 <400> SEQUENCE: 1
 29 gactaagctt ctgcatagtg agagaagacg 30
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 33 <211> LENGTH: 67
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Primer
 40 <400> SEQUENCE: 2
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 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Primer
 54 <400> SEQUENCE: 3
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 59 <211> LENGTH: 41
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Primer
 66 <400> SEQUENCE: 4

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73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Primer
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82 <210> SEQ ID NO: 6
83 <211> LENGTH: 31
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Primer
90 <400> SEQUENCE: 6
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94 <210> SEQ ID NO: 7
95 <211> LENGTH: 27
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
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100 <223> OTHER INFORMATION: Primer
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103 gttttcggcc gctgtccgtt cgtcttt 27
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107 <211> LENGTH: 27
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Primer
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118 <210> SEQ ID NO: 9
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121 <213> ORGANISM: Artificial Sequence
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132 <212> TYPE: DNA
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138 <400> SEQUENCE: 10
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155 <211> LENGTH: 3342
156 <212> TYPE: DNA
157 <213> ORGANISM: Bacillus licheniformis
159 <220> FEATURE:
160 <221> NAME/KEY: CDS
161 <222> LOCATION: (1303)..(2469)
162 <223> OTHER INFORMATION:
165 <220> FEATURE:
166 <221> NAME/KEY: misc_feature
167 <222> LOCATION: (2685)..(2685)
168 <223> OTHER INFORMATION: n denotes an undetermined nucleotide
171 <400> SEQUENCE: 12
172 gcgtaccgtt aaagtgcgaac agcgggtttct tcctttttac atccatggat taaaaagggg 60
174 ttgaaaaaag gtgagaaaaa gctttgtttt gcttttaacg gggctgcatg taatccttat 120
176 gctttctgcc tgcggccaaa aatcgcaaga agatgttgtg acggggctcg acaagaaggc 180
178 aaaagaatac acgtcctata aggcaaaagc gaaaatgacc attgaaacgg ggaatgacc 240
180 gcaggagtac aacgtggaaa tctggcataa aaaaccttct ctttacgggg tctatttgga 300
182 aaaccggaaa aaagaccaga gccagggtgat cttgcgcaat gaaaacggcg tgtttgtttt 360
184 gactccgctg ctgaataaaa gcttccgctt tcacagcgac tggcccaata acagcagcca 420
186 ggtatactta ttogaatcgc tegttaaagga tgtcaaaaat gatggggaag cttctttttc 480
188 cgcaaaggat tcaaaataca tttttgaaac gaaaacgaat tatcagcata atcagatgct 540
190 gccgactcag gaaatcgttt tccataaaaa gaccatggct ccttcacatcg ttaaagtgat 600
192 ggataccgac cgcaaaccga tggtaaaggt tgagtttaca agctttgaat tcgataagcc 660
194 gctcgataaa gactcttttg atgaaaagaa aaatatgacg ctgtctcaaa ttgacgtagc 720
196 gacaagcgct gacgtgtcag actctttcgc tgtcaaaaac cgcctcgatg tgcctcaggg 780
198 cgtgaaaaag cttgaagaga aagagatggc gactgaagac ggcaaacgga tcgtcatcac 840
200 atatggcggg gaaaaatcct ttacattgat tcaggaaaaa gccgcgctcg ccaaaacatc 900
202 cacttccgta tccatgaacg gagagcccggt tgacctcggc ttacaggctg gcgcactgac 960
204 ggataaatcg ttgtcatgga catatgacgg agtcgattac tttatctcat cagaagatct 1020
206 ttctcaagat gaacttctga tggttgcaaa aagcatgcag ggacagtctt cgaaatagac 1080
208 tgtgccgtat ccggcagcct gttttccgcc cggaagcgga aagcaggctt ttttatattt 1140
210 gcgtcgcaag cgtatgattt cgacagcttt tccgtaaaaat gtataccgtg ccagcaattt 1200
212 ttcttttgtt cagggtgat gatcccgctgc aaaatttccc tttctccgaa ctttttagta 1260
214 tgatgggaag gacgagtga acaaggaaca ggaagtgtca tg atg agc tta aaa 1314
215 Met Ser Leu Lys
216 1
218 cca ttc tat aga aag aca tgg gcc gaa atc gat tta acg gct tta aaa 1362
219 Pro Phe Tyr Arg Lys Thr Trp Ala Glu Ile Asp Leu Thr Ala Leu Lys
220 5 10 15 20
222 gaa aac gtc cgc aat atg aag cgg cac atc ggc gag cat gtc cgc ctg 1410

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223 Glu Asn Val Arg Asn Met Lys Arg His Ile Gly Glu His Val Arg Leu
224          25          30          35
226 atg gcc gtc gtt aaa gcg aat gcc tac gga cac ggg gat gca cag gta 1458
227 Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Asp Ala Gln Val
228          40          45          50
230 gcg aag gcg gct ctt gca gaa ggg gcg tcc att ctt gct gtg gct tta 1506
231 Ala Lys Ala Ala Leu Ala Glu Gly Ala Ser Ile Leu Ala Val Ala Leu
232          55          60          65
234 ttg gat gaa gcg ctt tcg ctg agg gcg cag ggg att gaa gaa ccg att 1554
235 Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile Glu Glu Pro Ile
236          70          75          80
238 ctt gtc ctc ggt gca gtg ccg acc gaa tat gca agc att gcc gcg gaa 1602
239 Leu Val Leu Gly Ala Val Pro Thr Glu Tyr Ala Ser Ile Ala Ala Glu
240 85          90          95          100
242 aag cgc att atc gtg act ggc tac tcc gtc ggc tgg ctg aaa gac gtg 1650
243 Lys Arg Ile Ile Val Thr Gly Tyr Ser Val Gly Trp Leu Lys Asp Val
244          105          110          115
246 ctc ggt ttt ctg aat gag gcc gaa gct cct ctt gaa tat cat ttg aag 1698
247 Leu Gly Phe Leu Asn Glu Ala Glu Ala Pro Leu Glu Tyr His Leu Lys
248          120          125          130
250 atc gac acg ggc atg ggc cgc ctt ggc tgc aaa acg gaa gaa gag atc 1746
251 Ile Asp Thr Gly Met Gly Arg Leu Gly Cys Lys Thr Glu Glu Glu Ile
252          135          140          145
254 aaa gaa atg atg gag atg acc gaa tcg aac gat aag ctc aat tgt acg 1794
255 Lys Glu Met Met Glu Met Thr Glu Ser Asn Asp Lys Leu Asn Cys Thr
256          150          155          160
258 ggc gtg ttc act cat ttc gcc acg gcg gac gaa aag gac acc gat tat 1842
259 Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys Asp Thr Asp Tyr
260 165          170          175          180
262 ttc aac atg cat ctt gac cgc ttt aaa gag ctg atc agc ccc ttc ccg 1890
263 Phe Asn Met His Leu Asp Arg Phe Lys Glu Leu Ile Ser Pro Phe Pro
264          185          190          195
266 ctt gac cgt ttg atg gtg cat tcg tca aac agc gcc gcg ggt ctg cgc 1938
267 Leu Asp Arg Leu Met Val His Ser Ser Asn Ser Ala Ala Gly Leu Arg
268          200          205          210
270 ttc agg gaa cag cta ttt aat gcc gtc cgc ttc ggc atc ggc atg tac 1986
271 Phe Arg Glu Gln Leu Phe Asn Ala Val Arg Phe Gly Ile Gly Met Tyr
272          215          220          225
274 ggt ttg gcg ccg tca adc gaa ata aaa gac gag ctg ccg ttt cgt ctg 2034
275 Gly Leu Ala Pro Ser Thr Glu Ile Lys Asp Glu Leu Pro Phe Arg Leu
276          230          235          240
278 cgg gaa gtg ttt tcg ctt cat acc gaa ctc acc cat gtg aaa aaa att 2082
279 Arg Glu Val Phe Ser Leu His Thr Glu Leu Thr His Val Lys Lys Ile
280 245          250          255          260
282 aaa aaa ggc gag agc gtc agc tac ggg gcg aca tat aca gct cag cgc 2130
283 Lys Lys Gly Glu Ser Val Ser Tyr Gly Ala Thr Tyr Thr Ala Gln Arg
284          265          270          275
286 gac gaa tgg atc ggg aca gtc ccc gtc ggg tat gcc gac gga tgg ctg 2178
287 Asp Glu Trp Ile Gly Thr Val Pro Val Gly Tyr Ala Asp Gly Trp Leu

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288          280          285          290
290 agg cgc ctg gcc gga acg gaa gtg ctg atc gac gga aaa cgc caa aaa      2226
291 Arg Arg Leu Ala Gly Thr Glu Val Leu Ile Asp Gly Lys Arg Gln Lys
292          295          300          305
294 ata gca ggg aga atc tgc atg gac cag ttc atg att tcc ctt gcc gaa      2274
295 Ile Ala Gly Arg Ile Cys Met Asp Gln Phe Met Ile Ser Leu Ala Glu
296          310          315          320
298 gaa tac cct gtc ggc aca aag gtt acc ttg atc gga aag caa aaa gac      2322
299 Glu Tyr Pro Val Gly Thr Lys Val Thr Leu Ile Gly Lys Gln Lys Asp
300 325          330          335          340
302 gaa tgg atc tca gtc gac gaa atc gcc caa aat ttg cag acg atc aat      2370
303 Glu Trp Ile Ser Val Asp Glu Ile Ala Gln Asn Leu Gln Thr Ile Asn
304          345          350          355
306 tat gaa att acc tgt atg ata agt tca agg gtg ccc cgt atg ttt ttg      2418
307 Tyr Glu Ile Thr Cys Met Ile Ser Ser Arg Val Pro Arg Met Phe Leu
308          360          365          370
310 gaa aat ggg agt ata atg gaa ata agg aat ccg atc ttg cct gat caa      2466
311 Glu Asn Gly Ser Ile Met Glu Ile Arg Asn Pro Ile Leu Pro Asp Gln
312          375          380          385
314 tcc tgaaaattga tgaattagcg gaaaaacaac tttgcttgcg aaaagaataa      2519
315 Ser
318 tgatatgatt atgaatggaa tggatagagt gttgtatccg taagtttggt ggaggtgtat      2579
320 gtttttgtct gaatccagcg caacaactga aatattgatt cgcttgccag aagctttagt      2639
W--> 322 atcagaactg gatggtgtcg tcatgcgaga taaccgggag cagganatga actgatttta      2699
324 ccaagccaca aaaatgtagg aacgcgaacg caaaaaatcg acaaattcgg ggaatcgatg      2759
326 agaagcgggt atatggagat ggccaagatc caatttgaac atctcttctg aggetcaatt      2819
328 tgcagagtat gaggtgaaa acacagtaga gcgcttacta agcggtatgat aatcatttga      2879
330 ttgttaaacy cgcgatggtt tattttgctg aacctatctcc tgttggttggc tcagaacaag      2939
332 gcggggtgcy cccggtttta gtgattcaaa acaacatcgg caatcgcttc agcccaactg      2999
334 ctattgttgc agccataaca gcccaaatac agaaagcaaa attacctacc cacgtcgaaa      3059
336 ttgatgcgaa acgctacggt ttgaaagag actccggttat attgctcgaa caaattcgga      3119
338 cgattgacaa gcaaagatta acggacaaaa tcacccatct cgatgatgaa atgatggaaa      3179
340 aggtcaacga agccttacia atcagtttgg cactcattga tttttaatat tgatgaaagt      3239
342 tgctcgaggc gaaagagcaa ctttttttgt gttcaaaaat aacaatacga tataatggta      3299
344 actgttagtc ctaaaaatgt tagccagatg tagtcagggg gat      3342
347 <210> SEQ ID NO: 13
348 <211> LENGTH: 389
349 <212> TYPE: PRT
350 <213> ORGANISM: Bacillus licheniformis
353 <400> SEQUENCE: 13
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356 1          5          10          15
359 Thr Ala Leu Lys Glu Asn Val Arg Asn Met Lys Arg His Ile Gly Glu
360          20          25          30
363 His Val Arg Leu Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly
364          35          40          45
367 Asp Ala Gln Val Ala Lys Ala Ala Leu Ala Glu Gly Ala Ser Ile Leu
368          50          55          60
371 Ala Val Ala Leu Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 2685

Seq#:49; N Pos. 669

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:2639

L:1412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:660